AMENDMENTS TO CLAIMS

1.   (amended)   A method of identifying a function of a gene sequence of interest in a cell type comprising:

a)   ~~over-expressing~~ overexpressing all or part of said sequence in a first population of said cell type;

b)   inhibiting expression of said sequence in a second population of said cell type;

c)   detecting changes in one or more cellular factors in said first and second populations; and

d)   identifying [[a]] said function of said gene sequence of interest based on the identity of, or effect on, said one or more cellular factors.

2.   (original)   The method of claim 1 wherein said changes are increases and/or decreases in the expression of said cellular factors.

3.   (original)   The method of claim 1 wherein said changes are in the post-translational modifications of said cellular factors.

4.   (original)   The method of claim 3 wherein said changes are in the phosphorylation or glycosylation of said cellular factors.

5.   (original)   The method of claim 1 wherein said changes are in the activity of said cellular factors.

6.   (amended)   The method of claim 1 wherein said ~~over-expressing~~ overexpressing of said gene sequence in a first population is by use of a pseudotyped lentiviral vector that expresses said gene sequence.

7.   (amended)   The method of claim 1 wherein said inhibiting expression <u>of said gene</u> <u>sequence</u> in a second population is by use of a pseudotyped lentiviral vector capable of expressing all or part of said gene sequence in an antisense orientation.

8.   (amended)   The method of claim 1 wherein said inhibiting expression <u>of said gene</u> <u>sequence</u> in a second population is by use of a pseudotyped lentiviral vector capable of expressing one or more ribozymes against said gene sequence.

9.   (amended)   The method of claim 1 wherein said inhibiting expression <u>of said gene</u> <u>sequence</u> in a second population is by the generation of post-transcriptional gene silencing (PTGS) against said gene sequence.

10.   (original)   The method of claim 1 wherein said cell type is a primary cell.

11.   (original)   The method of claim 1 wherein said cell type is a cultured cell line.

12.   (original)   The method of claim 1 wherein said gene sequence of interest was previously identified as expressed in cells of said cell type.

13.   (original)   The method of claim 1 wherein said gene sequence of interest was not previously identified as expressed in cells of said cell type.

14.   (original)   The method of claim 1 wherein said gene sequence of interest encodes a product which modulates expression of said one or more cellular factors by binding to nucleic acids encoding, or regulating the expression of, said one or more cellular factors.

15.   (original)   The method of claim 12 wherein said gene sequence of interest encodes a transcriptional activator.

16.   (original)   The method of claim 12 wherein said gene sequence of interest encodes a transcriptional repressor.

17.   (original)   The method of claim 1 wherein said gene sequence of interest is a human sequence.

18.   (original)   The method of claim 1 wherein said cell type is a human cell type.

19.   (amended)   A method of altering the expression of one or more cellular factors in a cell comprising over-expressing overexpressing or inhibiting the expression of a gene sequence for which a function was identified by the method of claim 1.

20.   (amended)   A method of altering the phenotype of a cell comprising over-expressing overexpressing or inhibiting the expression of a gene sequence for which a function was identified by the method of claim 1.

21.   (amended)   A method of identifying a function of a gene sequence of interest in a cell heterologous to the cellular source of said sequence comprising:
        a)   over-expressing overexpressing all or part of said sequence in a first population of said cell type;
        b)   inhibiting expression of said sequence in a second population of said cell type;
        c)   detecting changes in one or more cellular factors in said first and second populations; and
        d)   identifying said function of said gene sequence of interest based on the identity of, or effect on, said one or more cellular factors.

22.   (new)   A method of detecting a change in one or more cellular factors in a cell due to the overexpression or inhibition of a gene sequence of interest in said cell, comprising:

    a)   overexpressing all or part of said gene sequence in a first population of said cell type;

    b)   inhibiting expression of said gene sequence in a second population of said cell type; and

    c)   detecting a change in one or more cellular factors in said first and second populations.

    23.   (new) The method of claim 22, further comprising:

    d)   identifying the function of said gene sequence of interest based on the identity of, or effect on, said one or more cellular factors.

    24.   (new) The method of claim 23, further comprising:

    e)   altering the expression of said one or more cellular factors in a third population of said cell type cell by overexpressing or inhibiting the expression of said gene of interest for which a function was identified in step d).

    25.   (new) The method of claim 23, further comprising:

    e)   altering the phenotype of a third population of said cell type by overexpressing or inhibiting the expression of said gene sequence of interest for which a function was identified in step d).

    26.   (new) The method of claim 22, wherein said cell is heterologous to the cellular source of said gene sequence of interest.

    27.   (new) The method of claim 22, wherein said cellular factor is a cellular gene product or a metabolite.

    28.   (new) The method of claim 27, wherein said cellular gene product is a protein or RNA.

29.   (new)   The method of claim 27, wherein said metabolite is a sugar or a lipid.